IN THE CLAIMS

Please amend the claims as follows. This listing of claims replaces all prior versions.

1. (Currently amended) A method of identifying a human subject having an increased sensitivity to warfarin, wherein a therapeutic dose of warfarin for the subject is lower than a therapeutic dose of warfarin for a normal subject, comprising detecting in the subject the presence of an allele of a single nucleotide polymorphism in the VKOR gene, wherein the allele of the single nucleotide polymorphism is correlated with increased sensitivity to warfarin, thereby identifying the subject having increased sensitivity to warfarin.

2. (Canceled).

3. (Currently amended) A method of identifying a human subject having increased sensitivity to warfarin, comprising:

a) correlating the presence of an allele of a single nucleotide polymorphism in the VKOR gene with increased sensitivity to warfarin; and

b) detecting the allele of the single nucleotide polymorphism of step (a) in the subject, thereby identifying a subject having increased sensitivity to warfarin.

4-17. (Canceled).

18. (Currently amended) A method of amplifying a segment of a VKOR genomic nucleotide sequence, wherein said segment is in a noncoding region of the nucleotide sequence, comprising:

a) choosing a first oligonucleotide primer from the 3′ end of the nucleotide sequence of SEQ ID NO:8;

b) choosing a second oligonucleotide primer from the 5′ end of the nucleotide sequence of SEQ ID NO:8;

c) adding said first primer and said second primer to a nucleic acid sample; and

d) amplifying a segment of the VKOR genomic nucleotide sequence defined by the first primer and the second primer, wherein said segment is in a noncoding region of the nucleotide sequence.

19. (Previously presented) The method of claim 18, wherein the amplified segment of step (d) is less than 100 base pairs in length.

20. (Previously presented) The method of claim 18, wherein the amplified segment of step (d) comprises a single nucleotide polymorphism.

21. (Previously presented) The method of claim 18, wherein the amplified segment of step (d) comprises an allele of a single nucleotide polymorphism that is correlated with increased sensitivity to warfarin.

22. (Currently amended) The method of claim 18, wherein the nucleic acid sample is from a subject ~~in need of warfarin therapy~~ for whom identification of an increase or decrease in warfarin sensitivity is desired.

23. (Previously presented) The method of claim 18, wherein the first oligonucleotide primer is at least 15 nucleotides in length.

24. (Previously presented) The method of claim 18, wherein the second oligonucleotide primer is at least 15 nucleotides in length.

25. (Currently amended) A method of amplifying a segment of a VKOR genomic nucleotide sequence, wherein said segment is in a noncoding region of the nucleotide sequence, comprising:

a) choosing a first oligonucleotide primer from the nucleotide sequence of SEQ ID NO:8;

b) choosing a second oligonucleotide primer from the nucleotide sequence of SEQ ID NO:8 that differs in nucleotide sequence from the first oligonucleotide primer;

c) adding said first primer and said second primer to a nucleic acid sample; and

d) amplifying a segment of the VKOR genomic nucleotide sequence defined by the first primer and the second primer, wherein said segment is in a noncoding region of the nucleotide sequence.

26. (Previously presented) The method of claim 25, wherein the amplified segment of step (d) is less than 100 base pairs in length.

27. (Previously presented) The method of claim 25, wherein the amplified segment of step (d) comprises a single nucleotide polymorphism.

28. (Previously presented) The method of claim 25, wherein the amplified segment of step (d) comprises an allele of a single nucleotide polymorphism that is correlated with increased sensitivity to warfarin.

29. (Currently amended) The method of claim 25, wherein the nucleic acid sample is from a subject ~~in need of warfarin therapy~~ for whom identification of an increase or decrease in warfarin sensitivity is desired.

30. (Previously presented) The method of claim 25, wherein the first oligonucleotide primer is at least 15 nucleotides in length.

31. (Previously presented) The method of claim 25, wherein the second oligonucleotide primer is at least 15 nucleotides in length.

32-45. (Canceled).